Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

1. -41. (Cancelled).

42. (Withdrawn) An aptamer that specifically binds to a target, the target being capable of binding to a target partner, wherein the binding of the aptamer to the target regulates the binding of the target to the target partner.

43. (Withdrawn) The aptamer of claim 42, wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner.

44. (Withdrawn) The aptamer of claim 42, wherein the target is a cell membrane receptor or a viral surface molecule.

45. (Withdrawn) A composition comprising the aptamer and the target of claim 42.

46. (Currently Amended) A method of identifying an aptamer that binds to a target, wherein the binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the following steps:

a) contacting a candidate mixture of nucleic acids with a target partner or target partner analog or both under conditions that favor specific binding between the nucleic acids and the target partner or target partner analog or both;

b) partitioning the bound nucleic acids from the unbound nucleic acids and retaining the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target and the target partner or target partner analog or both under conditions that disfavor efficient binding between the target and target partner or target partner analog or both;

d) partitioning nucleic acids bound to a target-target partner complex or a target-target partner analog complex from unbound nucleic acids; and

e) retaining the nucleic acids bound to the target-target partner complex or the target-target partner analog complex,

thereby identifying an aptamer that binds to a target wherein the binding of the aptamer to the

target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

47. (Currently Amended) A method of identifying an aptamer that binds to a target wherein the binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the following steps:

a) contacting a target-based pool of nucleic acid molecules having high affinity and specificity for the target with the target and a target partner or target partner analog or both under conditions that disfavor efficient binding between the target and a target partner or target partner analog or both, wherein the ~~target or~~ target partner or target partner analog is attached to a support;

b) partitioning nucleic acids bound to the support bound target partner or target partner analog from unbound nucleic acids; and

c) retaining the nucleic acids associated with the support bound target partner or target partner analog,

thereby identifying an aptamer that binds a target wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

48. (Previously Presented) The method of claim 46, wherein the candidate mixture of nucleic acids in step a) is a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

49. (Currently Amended) The method of claim 46 or 48, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex ~~and amplifying the removed nucleic acids~~.

50. (Currently Amended) The method of claim 47, wherein step c) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex ~~and amplifying the removed nucleic acids~~.

51. (Currently Amended) The method of claim 49, further comprising in step e)

amplifying the removed nucleic acid molecules and repeating steps a) to e).

52. (Currently Amended) The method of claim 50, further comprising repeating in step c) amplifying the removed nucleic acid molecules and repeating steps a) to c).

53. (Previously Presented) The method of claim 51, wherein the target partner or target partner analog or both are immobilized.

54. (Previously Presented) The method of claim 51, wherein the target-based pool is diversified.

55. (Currently Amended) The method of claim 47, wherein ~~the retaining~~ step (c) further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex by eluting the aptamer with an agonist competitor to the aptamer.

56. (Currently Amended) The method of claim 49, wherein ~~the retaining~~ step (e) further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex by eluting the aptamer with an agonist competitor to the aptamer.

57. (Currently Amended) The method of claim 49, wherein ~~the retaining~~ step (e) further comprises contacting the bound nucleic acids with excess free target.

58. (Withdrawn) An aptamer that specifically binds to the target, wherein the binding of the aptamer to the target regulates the binding of the target to the target partner and wherein the aptamer is obtainable by the method of claim 46.

59. (Withdrawn) The aptamer of claim 58, wherein the target is a cell surface receptor.

60. (Currently Amended) A method of identifying an aptamer that binds to a target, wherein the binding of the aptamer to the target increases the binding affinity of the target for a target partner, comprising the following steps:

a) contacting a candidate mixture of nucleic acids with a target partner or target partner analog or both under conditions that favor specific binding between the nucleic acids and the target partner or target partner analog or both;

b) partitioning the bound nucleic acids from the unbound nucleic acids and retaining the unbound nucleic acids;

c) binding the target to a target partner or target partner analog or both to form a target-target partner or target-target partner analog complex or both, and contacting the target-target partner or target-target partner analog complex or both with the unbound nucleic acids under conditions that favor specific binding between the nucleic acids and the target-target partner or target-target partner analog complex or both; and

d) removing nucleic acids with low binding affinity for the target partner or target partner analog complex; and

e) combining an agonist competitor with the nucleic acids bound to the complex~~;~~ and eluting the bound nucleic acids~~, and amplifying the eluted nucleic acids~~,

thereby identifying an aptamer that binds a target, wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

61. (Currently Amended) The method of claim 60, further comprising in step e) amplifying the eluted nucleic acids and repeating steps a) to e).

62. (Previously Presented) The method of claim 61, wherein the candidate mixture of nucleic acids in step a) is a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

63. (Previously Presented) The method of claim 62, wherein the target-based pool is diversified.

64. (Currently Amended) The method of ~~claim 62~~ claim 60, wherein the target-target partner complex or target-target partner analog complex is immobilized.

65. (Withdrawn) An aptamer that specifically binds to the target, wherein the binding of the aptamer to the target regulates the binding of the target to the target partner and wherein the aptamer is obtainable by the method of claim 60.

66. (Currently Amended) A method of identifying an aptamer that binds to a target wherein the binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the following steps:

a) contacting a candidate mixture of nucleic acids with a target partner or target partner analog or both ~~complex of the target and agonist competitor under conditions that favor specific binding~~;

b) partitioning the bound nucleic acids from the unbound nucleic acids and retaining the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target and the target partner or target partner analog or both under conditions that disfavor specific binding of the target to the target partner or target partner analog, ~~wherein the target is immobilized~~;

d) partitioning the unbound nucleic acids and the nucleic acids bound to either the target partner or target partner analog from the ~~bound~~ nucleic acids bound to the target-target partner complex or target-target partner analog complex or both; and

e) removing and retaining the ~~bound~~ nucleic acids ~~from the immobilized~~ bound to the target-target partner complex or target-target partner analog complex or both,

thereby identifying an aptamer that binds a target wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

67. (Cancelled)

68. (Cancelled)

69. (Currently Amended) A method of identifying an aptamer that binds to a target wherein the binding of the aptamer to the target increases the binding affinity of the target for a target partner, comprising the following steps:

a) binding the target to the target partner or target partner analog or both to form a target-target partner complex or target-target partner analog complex or both and contacting the target-target partner complex or target-target partner analog complex with a target-based pool of nucleic acid molecules having high affinity and specificity for the target under conditions that favor

specific binding between the nucleic acids and the target-target partner or target-target partner analog complex; and

b) removing nucleic acids with low binding affinity for the target-target partner or target-target partner analog complex; and

c) retaining ~~nucleic acids bound to~~ the target-target partner or target-target partner analog complex with bound nucleic acids; and

d) combining an agonist competitor with the nucleic acids bound to complex, eluting the bound nucleic acids, and amplifying the eluted nucleic acids,

thereby identifying an aptamer that binds, wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

70. (Currently Amended) The method of claim 69, further comprising the step of contacting a modified target, wherein the modified target is lacking a region or regions required for the ~~target~~-binding of the target to the target partner or target partner analog, with a ~~target-based~~ pool of nucleic acid molecules ~~having high affinity and specificity for the target under conditions that favor specific binding~~; partitioning the bound nucleic acids from the unbound nucleic acids and contacting the unbound nucleic acids with the complex in step a).

71. (New) The method of claim 70, wherein the pool of nucleic acid molecules comprises a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

72. (New) The method of claim 46, further comprising step f) screening the nucleic acids retained in step e) for a desired functional activity.

73. (New) The method of claim 46, further comprising the step of contacting a modified target, wherein the modified target is lacking a region or regions required for the binding of the target to the target partner or target partner analog, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids and contacting the unbound nucleic acids with the complex in step a).

74. (New) The method of claim 73, wherein the pool of nucleic acid molecules comprises

a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

75. (New) The method of claim 46, wherein the binding of the aptamer to the target exposes a portion of the target, wherein said exposed portion of the target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

76. (New) The method of claim 46, wherein the binding of the aptamer to the target induces a conformational change in the target which increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

77. (New) The method of claim 47, wherein the target partner or target partner analog or both are immobilized.

78. (New) The method of claim 47, wherein the target-based pool is diversified.

79. (New) The method of claim 47, wherein step (c) further comprises contacting the bound nucleic acids with excess free target.

80. (New) The method of claim 47, further comprising step d) screening the nucleic acids retained in step c) for a desired functional activity.

81. (New) The method of claim 47, further comprising the step of contacting a modified target, wherein the modified target is lacking a region or regions required for the binding of the target to the target partner or target partner analog, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids and contacting the unbound nucleic acids with the complex in step a).

82. (New) The method of claim 81, wherein the pool of nucleic acid molecules comprises a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

83. (New) The method of claim 47, wherein the binding of the aptamer to the target exposes a portion of the target, wherein said exposed portion of the target has an increased

binding affinity for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

84. (New) The method of claim 47, wherein the binding of the aptamer to the target induces a conformational change in the target which increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

85. (New) The method of claim 60, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex.

86. (New) The method of claim 60, wherein step (e) further comprises contacting the bound nucleic acids with excess free target.

87. (New) The method of claim 60, further comprising step f) screening the nucleic acids amplified in step e) for a desired functional activity.

88. (New) The method of claim 60, further comprising the step of contacting a modified target, wherein the modified target is lacking a region or regions required for the binding of the target to the target partner or target partner analog, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids and contacting the unbound nucleic acids with the complex in step a).

89. (New) The method of claim 88, wherein the pool of nucleic acid molecules comprises a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

90 (New) The method of claim 60, wherein the binding of the aptamer to the target exposes a portion of the target, wherein said exposed portion of the target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

91. (New) The method of claim 60, wherein the binding of the aptamer to the target

induces a conformational change in the target which increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

92. (New) The method of claim 66, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex.

93. (New) The method of claim 66, wherein step (e) further comprises contacting the bound nucleic acids with excess free target.

94. (New) The method of claim 66, further comprising step f) screening the nucleic acids retained in step e) for a desired functional activity.

95. (New) The method of claim 66, further comprising the step of contacting a modified target, wherein the modified target is lacking a region or regions required for the binding of the target to the target partner or target partner analog, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids and contacting the unbound nucleic acids with the complex in step a).

96. (New) The method of claim 95, wherein the pool of nucleic acid molecules comprises a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

97. (New) The method of claim 66, wherein the binding of the aptamer to the target exposes a portion of the target, wherein said exposed portion of the target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

98. (New) The method of claim 66, wherein the binding of the aptamer to the target induces a conformational change in the target which increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

99. (New) The method of claim 66, wherein the target partner or target partner analog or both are immobilized.

100. (New) The method of claim 66, further comprising in step e) amplifying the eluted nucleic acids and repeating steps a) to e).

101. (New) The method of claim 66, where step e) further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex by eluting the aptamer with an agonist competitor to the aptamer.

102. (New) The method of claim 66, wherein the candidate mixture of nucleic acids in step a) is a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

103. (New) The method of claim 102, wherein the target-based pool is diversified.

104. (New) The method of claim 69, wherein step d) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex.

105. (New) The method of claim 69, wherein step (d) further comprises contacting the bound nucleic acids with excess free target.

106. (New) The method of claim 69, further comprising step e) screening the nucleic acids amplified in step d) for a desired functional activity.

107. (New) The method of claim 69, wherein the binding of the aptamer to the target exposes a portion of the target, wherein said exposed portion of the target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

108. (New) The method of claim 69, wherein the binding of the aptamer to the target induces a conformational change in the target which increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is

not bound by the aptamer.

109. (New) The method of claim 69, wherein the target partner or target partner analog or both are immobilized.

110. (New) The method of claim 69, further comprising in step e) amplifying the eluted nucleic acids and repeating steps a) to e).

111. (New) The method of claim 69, where step e) further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex by eluting the aptamer with an agonist competitor to the aptamer.

112. (New) The method of claim 69, wherein the candidate mixture of nucleic acids in step a) is a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

113. (New) The method of claim 112, wherein the target-based pool is diversified.

114. (New) A method of identifying an aptamer that binds to a target-wherein the binding of the aptamer to the target increases the binding affinity of the target for a target partner comprising the following steps:

a) contacting a candidate mixture of nucleic acids with a complex of the target and an agonist competitor under conditions that favor specific binding between the nucleic acid and the target-agonist competitor complex;

b) partitioning the bound nucleic acids from the unbound nucleic acids and retaining the unbound nucleic acids;

c) contacting the unbound nucleic acids with the target and the target partner or target partner analog or both under conditions that disfavor specific binding of the target and the target partner or target partner analog;

d) partitioning the unbound nucleic acids from the bound nucleic acids; and

e) removing and retaining the bound nucleic acids from the target-target partner complex or target-target partner analog complex,

thereby identifying an aptamer that binds a target wherein the binding of the aptamer to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

115. (New) The method of claim 114, wherein the candidate mixture of nucleic acids in step a) is a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

116. (New) The method of claim 114, wherein step e) further comprises removing the retained nucleic acids from the target-target partner complex or target-target partner analog complex.

117. (New) The method of claim 114, wherein (e) further comprises removing the nucleic acid molecules from the target-target partner complex or target-target partner analog complex by eluting the aptamer with an agonist competitor to the aptamer.

118. (New) The method of claim 115, wherein the target-based pool is diversified.

119. (New) The method of claim 114, wherein step (e) further comprises contacting the bound nucleic acids with excess free target.

120. (New) The method of claim 114, wherein the target, the target partner or target partner analog or both in step c) is immobilized.

121. (New) The method of claim 114, further comprising step f) screening the nucleic acids retained in step e) for a desired functional activity.

122. (New) The method of claim 114, further comprising the step of contacting a modified target, wherein the modified target is lacking a region or regions required for the binding of the target to the target partner or target partner analog, with a pool of nucleic acid molecules; partitioning the bound nucleic acids from the unbound nucleic acids and contacting the unbound nucleic acids with the complex in step a).

123. (New) The method of claim 122, wherein the pool of nucleic acid molecules

comprises a target-based pool of nucleic acid molecules having high affinity and specificity for the target.

124. (New) The method of claim 114, wherein the binding of the aptamer to the target exposes a portion of the target, wherein said exposed portion of the target has an increased binding affinity for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

125. (New) The method of claim 114, wherein the binding of the aptamer to the target induces a conformational change in the target which increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner where the target is not bound by the aptamer.

126. (New) The method of claim 114, further comprising in step e) amplifying the eluted nucleic acids and repeating steps a) to e).